



# SEQUENCE LISTING

<110> POWDERJECT VACCINES, INC.

<120> METHOD

<130> 092633-0104

<140> PCT/US04/033391

<141> 2004-10-12

<150> 60/567,771

<151> 2004-05-05

<150> 60/526,571

<151> 2003-12-04

<150> 60/510,086

<151> 2003-10-10

<160> 19

<170> PatentIn Ver. 3.2

<210> 1

<211> 63

<212> PRT

<213> Influenza A virus

<400> 1

Met Lys Thr Ile Ile Ala Leu Ser Tyr Ile Leu Cys Leu Val Phe Ala  
1 5 10 15

Gln Lys Leu Pro Gly Asn Asp Asn Ser Thr Ala Thr Leu Cys Leu Gly  
20 25 30

His His Ala Val Ser Asn Gly Thr Leu Val Lys Thr Ile Thr Asn Asp  
35 40 45

Gln Ile Glu Val Thr Asn Ala Thr Glu Leu Val Gln Ser Ser Ser  
50 55 60

<210> 2

<211> 65

<212> PRT

<213> Influenza A virus

<400> 2

Met Ala Ser Lys Thr Ile Ile Ala Leu Ser Tyr Ile Leu Cys Leu Val  
1 5 10 15

Phe Ala Gln Lys Leu Pro Gly Asn Asp Asn Ser Thr Ala Thr Leu Cys  
20 25 30

Leu Gly His His Ala Val Ser Asn Gly Thr Leu Val Lys Thr Ile Thr  
35 40 45

Asn Asp Gln Ile Glu Val Thr Asn Ala Thr Glu Leu Val Gln Ser Ser  
50 55 60

Ser  
65

<210> 3  
<211> 62  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
consensus sequence

<400> 3  
Lys Thr Ile Ile Ala Leu Ser Tyr Ile Leu Cys Leu Val Phe Ala Gln  
1 5 10 15  
Lys Leu Pro Gly Asn Asp Asn Ser Thr Ala Thr Leu Cys Leu Gly His  
20 25 30  
His Ala Val Ser Asn Gly Thr Leu Val Lys Thr Ile Thr Asn Asp Gln  
35 40 45  
Ile Glu Val Thr Asn Ala Thr Glu Leu Val Gln Ser Ser Ser  
50 55 60

<210> 4  
<211> 3759  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
nucleotide vector sequence

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agccgtttct gtaatgaagg agaaaactca ccgaggcagt tccataggat ggcaagatcc 180  
tggtatcggg ctgcgattcc gactcgtcca acatcaatac aacctattaa tttcccctcg 240  
tcaaaaataa ggttatcaag tgagaaatca ccatgagtga cgactgaatc cggtgagaat 300  
ggcaaaagct tatgcatttc tttccagact tgttcaacag gccagccatt acgctcgtca 360  
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aatacgcgat cgctgttaaa aggacaatta caaacaggaa tcgaatgcaa ccggcgcagg 480  
aacactgcc a gcatcaac aatattttca cctgaatcag gatattcttc taatacctgg 540  
aatgctgttt tcccggggat cgcagtgggt agtaaccatg catcatcagg agtacggata 600  
aatgcttga tggtcggaa aggcataaat tccgtcagcc agtttagtct gaccatctca 660  
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cggtaaatgg cccgcctggc tgaccgcccc acgacccccg ccattgacg tcaataatga 1140  
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gtcgtataaa cccgcctcgg ttgacgcaaa ttggcggtag gcgtgtacgg tgggaggtct 1560  
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tgctccgaat	attgcctctc	acatctcgtc	aatctccgcg	aggactgggg	accctgtgac	1980
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gggtctgacg	ctcagtgga	cgaaaactca	cgtaaaggga	ttttggctcat	gagattatca	3600
aaaaggatct	tcacctagat	ccttttaaat	taaaaatgaa	gttttaaatc	aatctaaagt	3660
atatatgagt	aaacttggtc	tgacagttac	caatgcttaa	tcagtgaggc	acctatctca	3720
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<210> 5

<211> 1503

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic nucleotide construct

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cttgaacggt	ttgccgtgaa	cccaggcctg	ctggaaacat	ctgagggatg	tcgccagatc	180
ctggggcaat	tgcagccatc	cctccagacc	gggagtgaag	agctgaggtc	cttgtataac	240
acagtggcta	ccctctactg	cgtacaccag	aggatcgaga	ttaaggatac	caaggaggcc	300
ttggacaaaa	ttgaggagga	gcaaaaacaag	agcaagaaga	aggcccagca	ggcagctgct	360
gacactgggc	atagcaacca	ggtatcacag	aactatccta	ttgtccaaaa	cattcagggc	420
cagatggttc	atcaggccat	cagcccccg	acgctcaatg	cctgggtgaa	ggttgtcgaa	480
gagaaggcct	tttctcctga	ggttatcccc	atgttctccg	ctttgagtga	ggggggccact	540
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ttgaaggaga	ctatcaacga	ggaggcagcc	gagtgggaca	gagtgcattc	cgtccacgct	660
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atctataaat	ggtggatcat	tctcggctct	aataaaaattg	ttagaatgta	ctctccgaca	840
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ctcctggtac	agaacgctaa	ccccgactgc	aaaacaatct	tgaaggcact	aggcccggtc	1020
gccaccctgg	aagagatgat	gaccgcctgt	cagggagtag	gcggacccgg	acacaaagcc	1080
agagtgttgg	ccgaagccat	gagccagggtg	acgaactccg	caaccatcat	gatgcagaga	1140
gggaaccttc	gcaatcagcg	gaagatcgtg	aagtgtttca	attgcggcaa	ggagggtcat	1200
accgcccgca	actgtcgggc	ccctaggaag	aaagggtggt	gggaagtgcg	caaggaggga	1260
caccagatga	aagactgtac	agaacgacag	gccaattttc	ttggaaagat	ttggccgagc	1320

tacaagggga gacctggtaa tttcctgcaa agcaggcccc agcccaccgc cccccctgag 1380  
 gaatccttca ggtccggagt ggagaccaca acgcctcccc aaaaacagga accaatcgac 1440  
 aaggagctgt accctttaac ttctctgcgt tctctcttg gcaacgacc gtcgtctcaa 1500  
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<210> 6  
 <211> 500  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic protein construct

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 Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys  
                     20                    25                    30  
 His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro  
                     35                    40                    45  
 Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu  
                     50                    55                    60  
 Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn  
                     65                    70                    75                    80  
 Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp  
                     85                    90                    95  
 Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys  
                     100                    105                    110  
 Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Asn Gln Val  
                     115                    120                    125  
 Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His  
                     130                    135                    140  
 Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu  
                     145                    150                    155                    160  
 Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser  
                     165                    170                    175  
 Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly  
                     180                    185                    190  
 Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu  
                     195                    200                    205  
 Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala  
                     210                    215                    220  
 Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr  
                     225                    230                    235                    240  
 Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile  
                     245                    250                    255  
 Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys

260	265	270
Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly		
275	280	285
Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu		
290	295	300
Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr		
305	310	315
Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala		
	325	330
Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly		
	340	345
Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser		
	355	360
Gln Val Thr Asn Ser Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg		
	370	375
Asn Gln Arg Lys Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His		
385	390	395
Thr Ala Arg Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys		
	405	410
Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn		
	420	425
Phe Leu Gly Lys Ile Trp Pro Ser Tyr Lys Gly Arg Pro Gly Asn Phe		
	435	440
Leu Gln Ser Arg Pro Glu Pro Thr Ala Pro Pro Glu Glu Ser Phe Arg		
	450	455
Ser Gly Val Glu Thr Thr Thr Pro Pro Gln Lys Gln Glu Pro Ile Asp		
465	470	475
Lys Glu Leu Tyr Pro Leu Thr Ser Leu Arg Ser Leu Phe Gly Asn Asp		
	485	490
Pro Ser Ser Gln		
500		

<210> 7

<211> 1515

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic nucleotide construct

<400> 7

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ctagaacgat	tcgcagttaa	tcctggcctg	ttagaaacat	cagaaggctg	tagacaaata	180
ctgggacagc	tacaaccatc	ccttcagaca	ggatcagaag	aacttagatc	attatataat	240
acagtagcaa	ccctctattg	tgtgcatcaa	aggatagaga	taaaagacac	caaggaagct	300
ttagacaaga	tagaggaaga	gcaaaacaaa	agtaagaaaa	aagcacagca	agcagcagct	360
gacacaggac	acagcaatca	ggtcagccaa	aattacccta	tagtgcagaa	catccagggg	420

caaatgggtac	atcaggccat	atcacctaga	acttttaa	catgggtaaa	agtagtagaa	480
gagaaggctt	tcagcccaga	agtataccc	atgttttcag	cattatcaga	aggagccacc	540
ccacaagatt	taaacacccat	gctaaacaca	gtggggggac	atcaagcagc	catgcaaatg	600
ttaaaagaga	ccatcaatga	ggaagctgca	gaatgggata	gagtgcattc	agtgcattgca	660
gggcctattg	caccaggcca	gatgagagaa	ccaaggggaa	gtgacatagc	aggaactact	720
agtacccttc	aggaacaaat	aggatggatg	acaaataatc	cacctatccc	agtaggagaa	780
atttataaaa	gatggataat	cctgggatta	aataaaatag	taagaatgta	tagccctacc	840
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tataaaactc	taagagccga	gcaagcttca	caggaggtaa	aaaattggat	gacagaaacc	960
ttgttgggtc	aaaatgcgaa	cccagattgt	aagactatgt	taaaagcatt	gggaccagcg	1020
gctacactag	aagaaatgat	gacagcatgt	cagggagtag	gaggaccccg	ccataaggca	1080
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tcccaaagaa	gacaagatat	ccttgatctg	tggatctacc	acacacaagg	ctacttcctc	1260
gattggcaga	actacacacc	agggccaggg	gtcagatatc	cactgacctt	tggatggtgc	1320
tacaagctag	taccagttga	gccagataag	gtagaagagg	ccaataaagg	agagaacacc	1380
agcttggtac	accctgtgag	cctgcatggg	atggatgacc	cggagagaga	agtgttagag	1440
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<210> 8

<211> 504

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic protein construct

<400> 8

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Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys	Lys	Lys	Tyr	Lys	Leu	Lys
			20					25					30		
His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu	Arg	Phe	Ala	Val	Asn	Pro
			35				40				45				
Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg	Gln	Ile	Leu	Gly	Gln	Leu
	50					55					60				
Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu	Leu	Arg	Ser	Leu	Tyr	Asn
	65			70						75					80
Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln	Arg	Ile	Glu	Ile	Lys	Asp
			85					90						95	
Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	Gln	Asn	Lys	Ser	Lys	
			100				105					110			
Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr	Gly	His	Ser	Asn	Gln	Val
		115				120						125			
Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile	Gln	Gly	Gln	Met	Val	His
	130				135						140				
Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Val	Glu
	145				150				155						160
Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu	Ser
			165					170						175	
Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly

180										185					190				
Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu	Glu				
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Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val	His	Ala	Gly	Pro	Ile	Ala				
	210					215					220								
Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr	Thr				
225					230					235					240				
Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	Asn	Asn	Pro	Pro	Ile				
			245						250					255					
Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn	Lys				
			260					265					270						
Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg	Gln	Gly				
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Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys	Thr	Leu				
	290					295					300								
Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Glu	Thr				
305					310					315					320				
Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Lys	Ala				
			325						330					335					
Leu	Gly	Pro	Ala	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln	Gly				
			340					345					350						
Val	Gly	Gly	Pro	Gly	His	Lys	Ala	Arg	Val	Leu	Val	Gly	Phe	Pro	Val				
		355					360					365							
Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro	Met	Thr	Tyr	Lys	Ala	Ala	Val	Asp				
	370					375					380								
Leu	Ser	His	Phe	Leu	Lys	Glu	Lys	Gly	Gly	Leu	Glu	Gly	Leu	Ile	His				
385					390					395					400				
Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu	Asp	Leu	Trp	Ile	Tyr	His	Thr	Gln				
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Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn	Tyr	Thr	Pro	Gly	Pro	Gly	Val	Arg				
			420					425					430						
Tyr	Pro	Leu	Thr	Phe	Gly	Trp	Cys	Tyr	Lys	Leu	Val	Pro	Val	Glu	Pro				
		435					440					445							
Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys	Gly	Glu	Asn	Thr	Ser	Leu	Leu	His				
	450					455					460								
Pro	Val	Ser	Leu	His	Gly	Met	Asp	Asp	Pro	Glu	Arg	Glu	Val	Leu	Glu				
465					470					475					480				
Trp	Arg	Phe	Asp	Ser	His	Leu	Ala	Phe	His	His	Val	Ala	Arg	Glu	Leu				
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His	Pro	Glu	Tyr	Phe	Lys	Asn	Cys												
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<210> 9  
 <211> 1518

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
nucleotide construct

<400> 9  
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ctgcgcccgg gaggcaaaaa gaaatacaag ctcaagcata tcgtgtgggc ctcgagggag 120  
cttgaacggt ttgccgtgaa cccaggcctg ctggaaacat ctgagggatg tcgccagatc 180  
ctggggcaat tgcagccatc cctccagacc gggagtgaag agctgaggtc cttgtataac 240  
acagtggcta cccttactg cgtacaccag aggatcgaga ttaaggatac caaggaggcc 300  
ttggacaaaa ttgaggagga gcaaaacaag agcaagaaga aggccagca ggcagctgct 360  
gacactgggc atagcaacca ggtatcacag aactatccta ttgtccaaaa cattcagggc 420  
cagatgggtc atcaggccat cagcccccg acgctcaatg cctgggtgaa ggttgtcgaa 480  
gagaaggcct tttctcctga gggtatcccc atgttctccg ctttgagtga gggggccact 540  
cctcaggacc tcaatacaat gcttaatacc gtgggcggcc atcaggccgc catgcaaatg 600  
ttgaaggaga ctatcaacga ggaggcagcc gagtgggaca gagtgcattc cgtccacgct 660  
ggcccaatcg cgcccgga ca gatgcgggag cctcgcggt ctgacattgc cggcaccacc 720  
tctactctgc aagagcaaat cggatggatg accaacaatc ctcccatccc agttggagaa 780  
atctataaac ggtggatcat tctcggctct aataaaaattg ttagaatgta ctctccgaca 840  
tccatccttg acattagaca gggaccacaa gagcctttta gggattacgt cgaccgggtt 900  
tataagaccc tgcgagcaga gcaggcctct caggaggtca aaaactggat gacggagaca 960  
ctcctggtac agaacgctaa ccccgactgc aaaacaatct tgaaggcact aggcccggt 1020  
gccaccctgg aagagatgat gaccgcctgt caggagtag gcggacccgg acacaaagcc 1080  
agagtgttga tgggtgggtt tccagtcaca cctcaggtag ctttaagacc aatgacttac 1140  
aaggcagctg tagatcttag ccacttttta aaagaaaagg ggggactgga agggctaatt 1200  
cactcccaaa gaagacaaga tatccttgat ctgtggatct accacacaca aggctacttc 1260  
cctgattggc agaactacac accagggccca ggggtcagat atccactgac ctttggatgg 1320  
tgctacaagc tagtaccagt tgagccagat aaggtagaag aggccataa aggagagaac 1380  
accagcttgt tacaccctgt gagcctgcat gggatggatg acccgagag agaatgttta 1440  
gagtggagg ttgacagcca cctagcattt catcacgtgg cccgagagct gcatccggag 1500  
tacttcaaga actgctga 1518

<210> 10  
<211> 505  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
protein construct

<400> 10  
Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp  
1 5 10 15  
Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys  
20 25 30  
His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro  
35 40 45  
Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu  
50 55 60  
Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn  
65 70 75 80  
Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp  
85 90 95  
Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys



100					105					110					
Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr	Gly	His	Ser	Asn	Gln	Val
		115					120					125			
Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile	Gln	Gly	Gln	Met	Val	His
	130					135					140				
Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Val	Glu
145					150					155					160
Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu	Ser
				165					170					175	
Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly
			180					185					190		
Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu	Glu
		195					200					205			
Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val	His	Ala	Gly	Pro	Ile	Ala
	210					215					220				
Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr	Thr
225					230					235					240
Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	Asn	Asn	Pro	Pro	Ile
			245						250					255	
Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn	Lys
		260						265					270		
Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg	Gln	Gly
		275					280					285			
Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys	Thr	Leu
	290					295					300				
Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Glu	Thr
305					310					315					320
Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Lys	Ala
			325						330					335	
Leu	Gly	Pro	Ala	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln	Gly
		340					345						350		
Val	Gly	Gly	Pro	Gly	His	Lys	Ala	Arg	Val	Leu	Met	Val	Gly	Phe	Pro
		355					360					365			
Val	Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro	Met	Thr	Tyr	Lys	Ala	Ala	Val
	370					375					380				
Asp	Leu	Ser	His	Phe	Leu	Lys	Glu	Lys	Gly	Gly	Leu	Glu	Gly	Leu	Ile
385					390					395					400
His	Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu	Asp	Leu	Trp	Ile	Tyr	His	Thr
			405						410					415	
Gln	Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn	Tyr	Thr	Pro	Gly	Pro	Gly	Val
		420						425					430		
Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Trp	Cys	Tyr	Lys	Leu	Val	Pro	Val	Glu
		435					440					445			

Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu Asn Thr Ser Leu Leu  
450 455 460

His Pro Val Ser Leu His Gly Met Asp Asp Pro Glu Arg Glu Val Leu  
465 470 475 480

Glu Trp Arg Phe Asp Ser His Leu Ala Phe His His Val Ala Arg Glu  
485 490 495

Leu His Pro Glu Tyr Phe Lys Asn Cys  
500 505

<210> 11  
<211> 1689  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
nucleotide construct

<400> 11  
atgggccccca tcagtcccat cgagaccgtg ccggtgaagc tgaaacccgg gatggacggc 60  
cccaaggtca agcagtggcc actcaccgag gagaagatca aggccctggt ggagatctgc 120  
accgagatgg agaaagaggg caagatcagc aagatcgggc ctgagaaccc atacaacacc 180  
cccgtgtttg ccatcaagaa gaaggacagc accaagtggc gcaagctggt ggatttccgg 240  
gagctgaata agcggaccca ggatttctgg gaggtccagc tgggcatccc ccatccggcc 300  
ggcctgaaga agaagaagag cgtgaccgtg ctggacgtgg gcgacgctta cttcagcgtc 360  
cctctggacg aggactttag aaagtacacc gcctttacca tcccattctat caacaacgag 420  
acccctggca tcagatatca gtacaacgtc ctcccccagg gctggaaggg ctctcccggc 480  
atcttccaga gctccatgac caagatcctg gagccgtttc ggaagcagaa ccccgatata 540  
gtcatctacc agtacatgga cgacctgtac gtgggctctg acctggaaat cgggcagcat 600  
cgcacgaaga ttgaggagct gaggcagcat ctgctgagat ggggcctgac cactccggag 660  
aagaagcatc agaaggagcc gccatttcctg tggatgggct acgagctcca tcccgacaag 720  
tggaccgtgc agcctatcgt cctccccgag aaggacagct ggaccgtgaa cgacatccag 780  
aagctggtgg gcaagctcaa ctgggctagc cagatctatc ccgggatcaa ggtgcgccag 840  
ctctgcaagc tgctgcgcgg caccaaggcc ctgaccgagg tgattcccct cacggaggaa 900  
gccgagctcg agctggctga gaaccgggag atcctgaagg agcccgtgca cggcgtgtac 960  
tatgaccctt ccaaggacct gatcgccgaa atccagaagc agggccaggg gcagtggaca 1020  
taccagattt accaggagcc tttcaagaac ctcaagaccg gcaagtacgc ccgcatgagg 1080  
ggcgcccaca ccaacgatgt caagcagctg accgaggccg tccagaagat cacgaccgag 1140  
tccatcgtga tctgggggaa gacacccaag ttcaagctgc ctatccagaa ggagacctgg 1200  
gagacgtggt ggaccgaata ttggcaggcc acctggattc ccgagtggga gttcgtgaat 1260  
acacctctct tgggtgaagct gtggtaccag ctcgagaagg agcccatcgt gggcgcgagg 1320  
acattctacg tggacggcgc ggccaaccgc gaaacaaagc tcgggaaggc cgggtacgtc 1380  
accaaccggg gccgcgagaa ggtcgtcacc ctgaccgaca ccaccaacca gaagacggag 1440  
ctgcaggcca tctatctcgc tctccaggac tccggcctgg aggtgaacat cgtgacggac 1500  
agccagtacg cgctgggcat tattcaggcc cagccggacc agtccgagag cgaactggtg 1560  
aaccagatta tcgagcagct gatcaagaaa gagaaggctt acctcgctg ggtcccggcc 1620  
cataagggca ttggcggcaa cgagcaggtc gacaagctgg tgagtgcggg gattagaaa 1680  
gtgctgttaa 1689

<210> 12  
<211> 562  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
protein construct

<400> 12  
Met Gly Pro Ile Ser Pro Ile Glu Thr Val Ser Val Lys Leu Lys Pro

1	5	10	15
Gly Met Asp Gly 20	Pro Lys Val Lys Gln 25	Trp Pro Leu Thr Glu 30	Glu Lys
Ile Lys Ala 35	Leu Val Glu Ile Cys 40	Thr Glu Met Glu Lys 45	Glu Gly Lys
Ile Ser 50	Lys Ile Gly Pro Glu 55	Asn Pro Tyr Asn Thr 60	Pro Val Phe Ala
Ile 65	Lys Lys Lys Asp Ser 70	Thr Lys Trp Arg Lys 75	Leu Val Asp Phe Arg 80
Glu Leu Asn Lys Arg 85	Thr Gln Asp Phe Trp 90	Glu Val Gln Leu Gly 95	Ile
Pro His Pro Ala 100	Gly Leu Lys Lys Lys 105	Lys Ser Val Thr Val 110	Leu Asp
Val Gly Asp Ala Tyr Phe Ser 115	Val 120	Pro Leu Asp Glu Asp 125	Phe Arg Lys
Tyr Thr Ala Phe Thr Ile Pro 130	Ser Ile Asn Asn Glu 140	Thr Pro Gly Ile	
Arg Tyr Gln Tyr Asn Val 150	Leu Pro Gln Gly Trp 155	Lys Gly Ser Pro Ala 160	
Ile Phe Gln Ser Ser 165	Met Thr Lys Ile Leu 170	Glu Pro Phe Arg Lys 175	Gln
Asn Pro Asp Ile Val Ile Tyr Gln 180	Tyr 185	Met Asp Asp Leu Tyr 190	Val Gly
Ser Asp Leu Glu Ile Gly Gln His 200	Arg Thr Lys Ile Glu 205	Glu Glu Leu Arg	
Gln His 210	Leu Leu Arg Trp Gly 215	Leu Thr Thr Pro Asp 220	Lys Lys His Gln
Lys Glu Pro Pro Phe Leu 230	Trp Met Gly Tyr Glu 235	Leu His Pro Asp Lys 240	
Trp Thr Val Gln Pro 245	Ile Val Leu Pro Glu 250	Lys Asp Ser Trp Thr 255	Val
Asn Asp Ile Gln Lys Leu Val Gly Lys 265	Leu Asn Trp Ala Ser 270	Gln Ile	
Tyr Pro Gly Ile Lys Val Arg Gln 280	Leu Cys Lys Leu 285	Leu Arg Gly Thr	
Lys Ala Leu Thr Glu Val Ile 295	Pro Leu Thr Glu Glu 300	Ala Glu Leu Glu	
Leu Ala Glu Asn Arg Glu 310	Ile Leu Lys Glu Pro 315	Val His Gly Val Tyr 320	
Tyr Asp Pro Ser Lys 325	Asp Leu Ile Ala Glu 330	Ile Gln Lys Gln Gly 335	Gln
Gly Gln Trp Thr Tyr Gln Ile Tyr Gln 345	Glu Pro Phe Lys Asn 350	Leu Lys	

Thr Gly Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys  
 355 360 365  
 Gln Leu Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile  
 370 375 380  
 Trp Gly Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp  
 385 390 395 400  
 Glu Thr Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp  
 405 410 415  
 Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu  
 420 425 430  
 Lys Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala  
 435 440 445  
 Asn Arg Glu Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Asn Arg Gly  
 450 455 460  
 Arg Gln Lys Val Val Thr Leu Thr Asp Thr Thr Asn Gln Lys Thr Glu  
 465 470 475 480  
 Leu Gln Ala Ile Tyr Leu Ala Leu Gln Asp Ser Gly Leu Glu Val Asn  
 485 490 495  
 Ile Val Thr Asp Ser Gln Tyr Ala Leu Gly Ile Ile Gln Ala Gln Pro  
 500 505 510  
 Asp Gln Ser Glu Ser Glu Leu Val Asn Gln Ile Ile Glu Gln Leu Ile  
 515 520 525  
 Lys Lys Glu Lys Val Tyr Leu Ala Trp Val Pro Ala His Lys Gly Ile  
 530 535 540  
 Gly Gly Asn Glu Gln Val Asp Lys Leu Val Ser Ala Gly Ile Arg Lys  
 545 550 555 560  
 Val Leu

<210> 13

<211> 1689

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
nucleotide construct

<400> 13

atgggccccca	tcagtccccat	cgagaccgtg	ccggtgaagc	tgaaacccgg	gatggacggc	60
cccaaggtca	agcagtggcc	actcaccgag	gagaagatca	aggccctggt	ggagatctgc	120
accgagatgg	agaaagaggg	caagatcagc	aagatcgggc	ctgagaaccc	atacaacacc	180
cccgtgtttg	ccatcaagaa	gaaggacagc	accaagtggc	gcaagctggt	ggatttcgg	240
gagctgaata	agcggaccca	ggatttctgg	gaggtccagc	tgggcatccc	ccatccggcc	300
ggcctgaaga	agaagaagag	cgtgaccgtg	ctggacgtgg	gcgacgctta	cttcagcgtc	360
cctctggacg	aggactttag	aaagtacacc	gcctttacca	tcccatctat	caacaacgag	420
acccctggca	tcagatatca	gtacaacgtc	ctccccaggg	gctggaaggg	ctctcccgcc	480
attttccaga	gctccatgac	caagatcctg	gagccgtttc	ggaagcagaa	ccccgatatc	540
gtcatctacc	agtacatgga	cgacctgtac	gtgggctctg	acctggaaat	cgggcagcat	600
gcacgaaga	ttgaggagct	gaggcagcat	ctgctgagat	ggggcctgac	cactccggac	660
aagaagcatc	agaaggagcc	gccattcctg	tggatgggct	acgagctcca	tcccgaaga	720

tgga	ccgtgc	agcctatcgt	cctccccgag	aaggacagct	ggaccgtgaa	cgacatccag	780
aagctgggtg	gcaagctcaa	ctgggctagc	cagatctatc	ccgggatcaa	ggtgcccag	840	
ctctgcaagc	tgctgcgcg	caccaaggcc	ctgaccgagg	tgattcccct	cacggaggaa	900	
gccgagctcg	agctggctga	gaaccgggag	atcctgaagg	agcccgtgca	cggcgtgtac	960	
tatgaccct	ccaaggacct	gatcgccgaa	atccagaagc	agggccaggg	gcagtggaca	1020	
taccagattt	accaggagcc	tttcaagaac	ctcaagaccg	gcaagtacgc	ccgcatgagg	1080	
ggcgcccaca	ccaacgatgt	caagcagctg	accgaggccg	tccagaagat	cacgaccgag	1140	
tccatcgta	tctgggggaa	gacaccaag	ttcaagctgc	ctatccagaa	ggagacctgg	1200	
gagacgtggt	ggaccgaata	ttggcaggcc	acctggattc	ccgagtggga	gttcgtgaat	1260	
acacctctc	tgggtgaagct	gtggtaccag	ctcgagaagg	agcccatcgt	gggcgcggag	1320	
acattctacg	tggacggcgc	ggccaaccgc	gaaacaaagc	tcgggaaggc	cgggtacgtc	1380	
accaaccggg	gccgccagaa	ggtcgtcacc	ctgaccgaca	ccaccaacca	gaagacggag	1440	
ctgcaggcca	tctatctcgc	tctccaggac	tccggcctgg	aggtgaacat	cgtgacggac	1500	
agccagtacg	cgctgggcat	tattcaggcc	cagccggacc	agtccgagag	cgaactggtg	1560	
aaccagatta	tcgagcagct	gatcaagaaa	gagaaggctc	acctcgcctg	ggtcccggcc	1620	
cataagggca	ttggcggcaa	cgagcaggtc	gacaagctgg	tgagtgcggg	gattagaaa	1680	
gtgctgtaa						1689	

<210> 14

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic protein construct

<400> 14

Met	Gly	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Ser	Val	Lys	Leu	Lys	Pro
1				5					10					15	
Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	Lys
		20						25					30		
Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	Lys
		35					40					45			
Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	Ala
	50					55					60				
Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	Arg
	65				70					75					80
Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	Ile
			85						90					95	
Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	Asp	
			100				105					110			
Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Glu	Asp	Phe	Arg	Lys
		115					120					125			
Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	Ile
	130					135					140				
Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	Ala
	145				150					155					160
Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	Gln
			165						170					175	
Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	Gly
			180				185						190		

Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg  
 195 200 205  
 Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His Gln  
 210 215 220  
 Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys  
 225 230 235 240  
 Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val  
 245 250 255  
 Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile  
 260 265 270  
 Tyr Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr  
 275 280 285  
 Lys Ala Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu  
 290 295 300  
 Leu Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr  
 305 310 315 320  
 Tyr Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln  
 325 330 335  
 Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys  
 340 345 350  
 Thr Gly Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys  
 355 360 365  
 Gln Leu Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile  
 370 375 380  
 Trp Gly Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp  
 385 390 395 400  
 Glu Thr Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp  
 405 410 415  
 Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu  
 420 425 430  
 Lys Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala  
 435 440 445  
 Asn Arg Glu Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Asn Arg Gly  
 450 455 460  
 Arg Gln Lys Val Val Thr Leu Thr Asp Thr Thr Asn Gln Lys Thr Glu  
 465 470 475 480  
 Leu Gln Ala Ile Tyr Leu Ala Leu Gln Asp Ser Gly Leu Glu Val Asn  
 485 490 495  
 Ile Val Thr Asp Ser Gln Tyr Ala Leu Gly Ile Ile Gln Ala Gln Pro  
 500 505 510  
 Asp Gln Ser Glu Ser Glu Leu Val Asn Gln Ile Ile Glu Gln Leu Ile  
 515 520 525  
 Lys Lys Glu Lys Val Tyr Leu Ala Trp Val Pro Ala His Lys Gly Ile  
 530 535 540

Gly Gly Asn Glu Gln Val Asp Lys Leu Val Ser Ala Gly Ile Arg Lys  
545 550 555 560

Val Leu

<210> 15

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 15

Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu  
1 5 10

<210> 16

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 16

Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Ile Thr Gly Lys  
1 5 10 15

<210> 17

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 17

cgccactctc ttccgacacc

20

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 18

ccaagaacat cacacggaac c

21

<210> 19

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 19

His Gly Pro Ser Leu Tyr Arg Thr Phe  
1 5